

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
 Tang, Y. Tom
 Corley, Neil C.
 Guegler, Karl J.
 Yue, Henry
 Patterson, Chandra

(ii) TITLE OF THE INVENTION: PROTEINS ASSOCIATED WITH EGF SIGNALING

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Genomics, Inc.
 (B) STREET: 3160 Porter Dr.
 (C) CITY: Palo Alto
 (D) STATE: CA
 (E) COUNTRY: USA
 (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
 (B) FILING DATE: Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/069,725
 (B) FILING DATE: April 29, 1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
 (B) REGISTRATION NUMBER: 36,749
 (C) REFERENCE/DOCKET NUMBER: PF-0515-1 CON

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
 (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: COLNNOT16
 (B) CLONE: 1281694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asn Asp Ser Leu Arg Thr Asp Val Phe Val Arg Phe Gln Pro Glu
 1 5 10 15

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Ser Ile Ala Cys Ala Cys Ile Tyr Leu Ala Ala Arg Thr Leu Glu Ile
 20 25 30
 Pro Leu Pro Asn Arg Pro His Trp Phe Leu Leu Phe Gly Ala Thr Glu
 35 40 45
 Glu Glu Ile Gln Glu Ile Cys Leu Lys Ile Leu Gln Leu Tyr Ala Arg
 50 55 60
 Lys Lys Val Asp Leu Thr His Leu Glu Gly Glu Val Glu Lys Arg Lys
 65 70 75 80
 His Ala Ile Glu Glu Ala Lys Ala Gln Ala Arg Gly Leu Leu Pro Gly
 85 90 95
 Gly Thr Gln Val Leu Asp Gly Thr Ser Gly Phe Ser Pro Ala Pro Lys
 100 105 110
 Leu Val Glu Ser Pro Lys Glu Gly Lys Gly Ser Lys Pro Ser Pro Leu
 115 120 125
 Ser Val Lys Asn Thr Lys Arg Arg Leu Glu Gly Ala Lys Lys Ala Lys
 130 135 140
 Ala Asp Ser Pro Val Asn Gly Leu Pro Lys Gly Arg Glu Ser Arg Ser
 145 150 155 160
 Arg Ser Arg Ser Arg Glu Gln Ser Tyr Ser Arg Ser Pro Ser Arg Ser
 165 170 175
 Ala Ser Pro Lys Arg Arg Lys Ser Asp Ser Gly Ser Thr Ser Gly Gly
 180 185 190
 Ser Lys Ser Gln Ser Arg Ser Arg Ser Arg Ser Asp Ser Pro Pro Arg
 195 200 205
 Gln Ala Pro Arg Ser Ala Pro Tyr Lys Gly Ser Glu Ile Arg Gly Ser
 210 215 220
 Arg Lys Ser Lys Asp Cys Lys Tyr Pro Gln Lys Pro His Lys Ser Arg
 225 230 235 240
 Ser Arg Ser Ser Ser Arg Ser Arg Ser Arg Ser Arg Glu Arg Ala Asp
 245 250 255
 Asn Pro Gly Lys Tyr Lys Lys Lys Ser His Tyr Tyr Arg Asp Gln Arg
 260 265 270
 Arg Glu Arg Ser Arg Ser Tyr Glu Arg Thr Gly Arg Arg Tyr Glu Arg
 275 280 285
 Asp His Pro Gly His Ser Arg His Arg Arg
 290 295

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3464 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT16
 (B) CLONE: 1281694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTCGTGAAGC	ACTCCATGGA	GCATGTGTCA	ATGGCCTGTG	TCCACCTGGC	TTCCAAGATA	60
GAAGAGGCC	CAAGACGCAT	ACGGGACGTC	ATCAATGTGT	TTCACCGCCT	TCGACAGCTG	120
AGAGACAAA	AATAATCGTT	ATGTACCTTC	AGGTGTTAGA	GTGTGAGCGT	AACCAACACC	180
TGGTCCAGAC	CTCATGGGTA	GCCTCTGAGG	GTAAGTGA	AAGACTTCTC	CTCTGCTGTC	240
CAAGCGCTTT	GGTGCAGGGA	CAGCGGCATC	TTCAGCCAAT	CCAGTGCAGG	CTCTCCACCG	300
AAGGCTGGCT	CTAGACTGGT	GACCCCTTGT	TGAAATGGGA	CAGTTGGCAG	CGGCTCTGAT	360
GAGCCCCGAGA	AGAGGCCTGC	CCTTGGGTGC	GGAGTCTCCC	TCCGCACGAT	GCTCCACGC	420
GTCCAACCTTG	CACCCAAGGG	GCTTTTCCCT	CTTCCAAGTG	GACTCCTTCA	AGGAAGCTGC	480
AGCTCGGTCA	GCAGAGAAGG	GGCCTGCCGC	CAGCGCCCTG	GAGGAAGAGG	AAGAGGAACC	540
CAAGAGGATG	GCTTGTCTCC	CAGCAGCCAC	ACCGGCTTTG	TGCTCAGCCA	GTTCATTTGA	600
GTTTGCATGT	TTCTCTGCAC	TATGGATTTT	GAGCATTTAG	ATTTCTTTAA	TCAAAAGCGT	660
TTTAGTGA	CCAGTAGACA	TTTTCTTTCT	GAGGCATCGT	GCTTTGCATG	AGAGCAGGCC	720
AAGGTTGAGG	GGAAAAGTAA	AGTTAAAGTC	GGTTCTCTTT	CATAGCAACA	CGTATTGTCT	780
GACATTCAGC	CAGCTTTTTT	TTTTTCTAAT	AATTTCTGTG	CCTTTCTGTC	CTGTATTTAC	840
TGTATTTAGA	AAAAGCAGCT	AGAATATTTT	TCCATTA	CTTGAGATT	ACAGGACTGT	900

CTAGCTCTGA	GTCCTAGCAA	TAGACTCCTT	AGAGGAGTAG	TACGTTTATC	TAGATTTTCT	960
CTAGATAATG	CAGGCGGAAG	ACCTGGGTTC	CCGGGTGGGG	CATTGCAGTT	CTTCCTGTGT	1020
TTGGCTTCCA	GGAATTACAT	GAACGACAGC	CTTCGCACCG	ACGTCTTCGT	GCGGTTCCAG	1080
CCAGAGAGCA	TCGCCTGTGC	CTGCATTTAT	CTTGCTGCCC	GGACGCTGGA	GATCCCTTTG	1140
CCCAATCGTC	CCCATTTGGTT	TCTTTTGT	GGAGCAACTG	AAGAAGAAAT	TCAGGAAATC	1200
TGCTTAAAGA	TCTTGCAGCT	TTATGCTCGG	AAAAAGGTTG	ATCTCACACA	CCTGGAGGGT	1260
GAAGTGGAAA	AAAGAAAAGCA	CGCTATCGAA	GAGGCAAAGG	CCCAAGCCCC	GGGCTGTGTG	1320
CCTGGGGGCA	CACAGGTGCT	GGATGGTACC	TCGGGGTTCT	CTCCTGCCCC	CAAGCTGGTG	1380
GAATCCCCCA	AAGAAGGTAA	AGGGAGCAAG	CCTTCCCCAC	TGTCTGTGAA	GAACACCAAG	1440
AGGAGGCTGG	AGGGCGCCAA	GAAAGCCAAG	GCGGACAGCC	CCGTGAACGG	CTTGCCAAAG	1500
GGGCGAGAGA	GTCGGAGTCG	GAGCCGGAGC	CGTGAGCAGA	GCTACTCGAG	GTCCCCATCC	1560
CGATCAGCGT	CTCCTAAGAG	GAGGAAAAGT	GACAGCGGCT	CCACATCTGG	TGGGTCCAAG	1620
TCGCAGAGCC	GCTCCCGGAG	CAGGAGTGAC	TCCCCACCGA	GACAGGCCCC	CCGCAGCGCT	1680
CCCTACAAAG	GCTCTGAGAT	TCGGGGCTCC	CGGAAGTCCA	AGGACTGCAA	GTACCCCCAG	1740
AAGCCACACA	AGTCTCGGAG	CCGGAGTTCT	TCCCGTTCTC	GAAGCAGGTC	ACGGGAGCGG	1800
GCGGATAATC	CGGGAAAATA	CAAGAAGAAA	AGTCATTACT	ACAGAGATCA	GCGACGAGAG	1860
CGCTCGAGGT	CGTATGAACG	CACAGGCCGT	CGCTATGAGC	GGGACCACCC	TGGGCACAGC	1920
AGGCATCGGA	GGTGAGGCGG	GGTTGCAGTG	ACTGGTGGCC	GCAAGCCCTT	CCCTGGGGAG	1980
TACCTGATGG	CTGCCCTTTG	ACCCCCGGTG	GCTGCCCTTT	GACCCCCGGG	TGTGCTCTCA	2040
GCGCAAGTGG	TCCTAGAACA	GGATTCTTTT	TGGAAATGTC	TGTCGACTGG	ACCTTGGTGG	2100
ATTTGGAAAT	GGAAC TGAGG	GACCGGTGAC	ACGTGCTTCA	GACCGGTCTG	GGGTGCGGCG	2160
CACACCTGGG	CCCGTG CAGG	GCTCAGCTCG	GCAGCAGCTC	TGAGGGCAGC	TCAATGAAAA	2220
AGTGAATGCA	CACGCCCTTG	TTGGCGTG GC	CTGGCATGGC	CTGGTGCTAT	CGGCAGCCGC	2280
TCTCCACTCC	CCGACTGATA	CTCAATTACG	TGAAGCCAAG	AAAGATGATT	TTTAGAACCT	2340
TTGCCTATAT	TAGGTTGTAC	TTATGTACAT	ATTTTGCAGT	GTTTCACAGG	AGAAAGTGGC	2400
CTTAAC TGCC	CCTTATTC TC	TCTCCACGTT	GTAAATAAAC	ATGTGTTTAA	TACAAGTTAA	2460
AGCTATGTAT	GAAAACTCAG	AACTTGAATC	CCGTCAGCTT	AAAAC TTGTG	TAGGGAATCC	2520
TGACTTTTAA	AATGTGAGGG	TATTTGGATC	TGTGTTGAAA	GTCGTATATT	TTTATCTGTG	2580
CGGTGCTGAG	TGCAGGCCAC	CAGCTCCTAA	ATAGAGGTTC	CCTATATGCG	CGTATGACAT	2640
GGTGAATAAA	CACAACTCTC	TCCACTCAGG	ACATCCGGAG	CGTTATGGAC	GTGGTAGGTG	2700
GTCGTTCTGT	GTGCTTG TGA	AAGTGTCCAG	GCGTGTGCAC	AGCCAGTGCG	CCCACTTCCG	2760
GGCTCCTTGC	TCCCTGCTGT	ACTGAAGTTT	TGGATTTTGC	ATCCAATCCT	GTGTGCCTGC	2820
CCTTCTGCCG	AAGCTTGTGA	GGGGCCTGAG	TCCTCTGCCC	ATCAGGATGA	CAGGCTCCTT	2880
CCTGCAGGGC	CATAGGAGGG	AAGTTTTTGA	AACACAGAAT	GATTCCAAGG	TGCTCTCGTT	2940
CCTGAGGGGG	ACTGGTTTGT	AACCCATGAC	ATCTGTGGGC	GAGAGAGGCA	GCTGGGAGCA	3000
GGACACTTGG	AGGGTCACCC	CACGGGGGTG	GCACCTGCAC	TCTGAGTGCC	CCCCACTGTC	3060
ATCAGCTGCC	TCTTACCGTG	GACACAGTTT	TGGTTTTTGG	GACTAGGGGG	CCCCACTCCT	3120
GGTGGTACCG	TTTGGACTTA	CTAGGGCAGT	GGGACATATA	GGCCGGGGCT	AGTGGGATAA	3180
CGGGGAGTTA	CGCCTGATGA	CTTTTTTGAT	GGAATCCTGC	ATTAGATAGC	TGGTGGGACC	3240
CCCCCCTCAG	AATTTGGGGAA	CTGAGGAGAC	TCCAGGGAGG	GTGTCCTTCC	AGGGAGAGCA	3300
GCTATGAGGG	GCCCCCTAGC	TTCCCTGTGCC	TGGAAGTAAG	AGAACCAGTA	AAGGGCCATA	3360
CACACCTGTA	CCCAAGAGAC	CGCTCTCCAT	TTGCTTTCTT	TTTTTACTAA	ATAATTGTAA	3420
AATATTATTA	TGACATAAAG	AACCATT TAA	GGCCAAAAAA	AAAA		3464

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BEPINOT01
- (B) CLONE: 2056178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Tyr	Ser	Ala	Gln	Arg	Phe	Trp	Gly	Thr	Ile	Trp	Ala	Arg	Arg	Gly	1	5	10	15
Ala	His	Leu	Ala	Pro	Pro	Asp	Ala	Ser	Ile	Leu	Ile	Ser	Asn	Val	Cys	20	25	30	
Ser	Ile	Gly	Asp	His	Val	Ala	Gln	Glu	Leu	Phe	Gln	Gly	Ser	Asp	Leu	35	40	45	
Gly	Met	Ala	Glu	Glu	Ala	Glu	Arg	Pro	Gly	Glu	Lys	Ala	Gly	Gln	His	50	55	60	
Ser	Pro	Leu	Arg	Glu	Glu	His	Val	Thr	Cys	Val	Gln	Ser	Ile	Leu	Asp	65	70	75	80
Glu	Phe	Leu	Gln	Thr	Tyr	Gly	Ser	Leu	Ile	Pro	Leu	Ser	Thr	Asp	Glu	85	90	95	
Val	Val	Glu	Lys	Leu	Glu	Asp	Ile	Phe	Gln	Gln	Glu	Phe	Ser	Thr	Pro	100	105	110	
Ser	Arg	Lys	Gly	Leu	Val	Leu	Gln	Leu	Ile	Gln	Ser	Tyr	Gln	Arg	Met	115	120	125	
Pro	Gly	Asn	Ala	Met	Val	Arg	Gly	Phe	Arg	Val	Ala	Tyr	Lys	Arg	His	130	135	140	
Val	Leu	Thr	Met	Asp	Asp	Leu	Gly	Thr	Leu	Tyr	Gly	Gln	Asn	Trp	Leu	145	150	155	160
Asn	Asp	Gln	Val	Met	Asn	Met	Tyr	Gly	Asp	Leu	Val	Met	Asp	Thr	Val	165	170	175	
Pro	Glu	Lys	Val	His	Phe	Phe	Asn	Ser	Phe	Phe	Tyr	Asp	Lys	Leu	Arg	180	185	190	
Thr	Lys	Gly	Tyr	Asp	Gly	Val	Lys	Arg	Trp	Thr	Lys	Asn	Val	Asp	Ile	195	200	205	
Phe	Asn	Lys	Glu	Leu	Leu	Leu	Ile	Pro	Ile	His	Leu	Glu	Val	His	Trp	210	215	220	
Ser	Leu	Ile	Ser	Val	Asp	Val	Arg	Arg	Arg	Thr	Ile	Thr	Tyr	Phe	Asp	225	230	235	240
Ser	Gln	Arg	Thr	Leu	Asn	Arg	Arg	Cys	Pro	Lys	His	Ile	Ala	Lys	Tyr	245	250	255	
Leu	Gln	Ala	Glu	Ala	Val	Lys	Lys	Asp	Arg	Leu	Asp	Phe	His	Gln	Gly	260	265	270	
Trp	Lys	Gly	Tyr	Phe	Lys	Met	Asn	Val	Ala	Arg	Gln	Asn	Asn	Asp	Ser	275	280	285	
Asp	Cys	Gly	Ala	Phe	Val	Leu	Gln	Tyr	Cys	Lys	His	Leu	Ala	Leu	Ser	290	295	300	
Gln	Pro	Phe	Ser	Phe	Thr	Gln	Gln	Asp	Met	Pro	Lys	Leu	Arg	Arg	Gln	305	310	315	320
Ile	Tyr	Lys	Glu	Leu	Cys	His	Cys	Lys	Leu	Thr	Val					325	330		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BEPINOT01
(B) CLONE: 2056178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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GCCTCCCTGT CCCCCGACCC TCTTTTGTATG CCTCAGCAAG TGAAGAGGAG GAAGAAGAGG      60
AGGAGGAGGA GGATGAAGAT GAAGAGGAGG AAGTGGCAGC TTGGAGGCTG CCCCCAAGAT      120
GGAGTCAGCT GGGAACTTCC CAGCGGCCCC GCCCTTCCCG CCCCACATCAT CGAAAAACCT      180
GCTCACAGCG CCGCCGCCGA GCCATGAGAG CCTTCCGGAT GCTGCTCTAC TCAAAAAGCA      240
CCTCGCTGAC ATTCCACTGG AAGCTTTGGG GCGGCCACCG GGGCCGCGG CGGGGCTCG      300
CACACCCCAA GAACCATCTT TCACCCACAG AAGGGGGTGC GACGCCACAG GTGCCATCCC      360
CCTGTTGTGCG TTTTGACTCC CCCCAGGGGC CACCTCCACC CCGGCTGGGT CTGCTAGGTG      420
CTCTCATGGG TGAGGATGGG GTGAGAGGGT CTCCACCATG GCCCTCTGGG CCCCCATGG      480
AGGAAGATGG ACTCAGGTGG ACTCCAAAGT CTCTCTGGA CCCTGACTCG GGCCTCCTTT      540
CATGTACTCT GCCCAACGGT TTTGGGGGAC AATCTGGGCC AGAAGGGGAG CGCACTTGGC      600
ACCCCTGAT GCCAGCATCC TCATCAGCAA TGTGTGCAGC ATCGGGGACC ATGTGGCCCA      660
GGAGCTTTTT CAGGGCTCAG ATTTGGGCAT GGCAGAAGAG GCAGAGAGGC CTGGGGAGAA      720
AGCCGGCCAG CACAGCCCCC TGCAGAGGA GCATGTGACC TCGGTACAGA GCATCTTGGA      780
CGAATTCCTT CAAACGTATG GCAGCCTCAT ACCCCTCAGC ACTGATGAGG TAGTAGAGAA      840
GCTGGAGGAC ATTTTCCAGC AGGAGTTTTC CACCCCTTCC AGGAAGGGCC TGGTGTGCA      900
GCTGATCCAG TCTTACCAGC GGATGCCAGG CAATGCCATG GTGAGGGGCT TCCGAGTGGC      960
TTATAAGCGG CACGTGCTGA CCATGGATGA CTTGGGGACC TTGTATGGAC AGAACTGGCT      1020
CAATGACCAG GTGATGAACA TGTATGGAGA CCTGGTCATG GACACAGTCC CTGAAAAGGT      1080
GCATTTCTTC AATAGTTTCT TCTATGATAA ACTCCGTACC AAGGGTTATG ATGGGGTGAA      1140
AAGGTGGACC AAAAACGTGG ACATCTTCAA TAAGGAGCTA CTGCTAATCC CCATCCACCT      1200
GGAGGTGCAT TGGTCCCTCA TCTCTGTTGA TGTGAGGCGA CGCACCATCA CCTATTTTGA      1260
CTCGCAGCGT ACCCTAAACC GCGCTGCCC TAAGCATATT GCCAAGTATC TACAGGCAGA      1320
GGCGGTAAAG AAAGACCGAC TGGATTTCCA CCAGGGCTGG AAAGGTTACT TCAAAATGAA      1380
TGTGGCCAGG CAGAATAATG ACAGTGAAGT TGGTGTCTTT GTGTTGCAGT ACTGCAAGCA      1440
TCTGGCCCTG TCTCAGCCAT TCAGCTTCAC CCAGCAGGAC ATGCCCAAAC TTCGTCGGCA      1500
GATCTACAA GAGCTGTGTC ACTGCAAACT CACTGTGTGA GCCTCGTACC CCAGACCCCA      1560
AGCCCATAAA TGGGAAGGGA GACATGGGAG TCCCTTCCCA AGAAACTCCA GTTCCTTTCC      1620
TCTCTTGCTT CTTCCCACTC ACTTCCCTTT GGTTTTTTCAT ATTTAAATGT TTCAATTTCT      1680
GTATTTTTTT TTCTTTGAGA GAATACTTGT TGATTTCTGA TGTGCAGGGG GTGGCTACAG      1740
AAAAGCCCCT TTCTTCTCT GTTTGCAGGG GAGTGTGGCC CTGTGGCCTG GGTGGAGCAG      1800
TCATCTCTCC CTTTCCCCGT GCAGGGAGCA GGAAATCAGT GCTGGGGGTG GTGGGCGGAC      1860
AATAGGATCA CTGCCTGCCA GATCTTCAA CTTTTATATA TATATATATA TATATATATA      1920
TATATATATA TATATATATA TATATATATA AATATATAAA TGCCACGGTC CTGCTCTGGT      1980
CAATAAAGAT C

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
(B) CLONE: 1276645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Glu Gly Pro Lys Lys Ala Gln Gly His Ser Pro Val Asn Gly Leu
 1          5          10          15
Leu Lys Gly Gln Glu Ser Arg Ser Gln Ser Arg Ser Arg Glu Gln Ser
          20          25          30
Tyr Ser Arg Ser Pro Ser Arg Ser Ala Ser Pro Lys Arg Arg Lys Ser
          35          40          45
Asp Ser Gly Ser Thr Ser Gly Gly Ser Lys Ser Gln Ser Arg Ser Arg
          50          55          60
Ser Arg Ser Asp Ser Pro Pro Arg Gln Val His Arg Gly Ala Pro Tyr
          65          70          75          80
Lys Gly Ser Glu Val Arg Gly Ser Arg Lys Ser Lys Asp Cys Lys Tyr
          85          90          95

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PF-0515-1 CON

Leu	Thr	Gln	Lys	Pro	His	Lys	Ser	Arg	Ser	Arg	Ser	Ser	Ser	Arg	Ser	
			100					105					110			
Arg	Ser	Arg	Ser	Arg	Glu	Arg	Thr	Asp	Asn	Ser	Gly	Lys	Tyr	Lys	Lys	
		115					120					125				
Lys	Ser	His	Tyr	Tyr	Arg	Asp	Gln	Arg	Arg	Glu	Arg	Ser	Arg	Ser	Tyr	
	130					135					140					
Glu	Arg	Thr	Gly	His	Arg	Tyr	Glu	Arg	Asp	His	Pro	Gly	His	Ser	Arg	
145					150					155						160
His	Arg	Arg	Cys	Asp	Arg	Ile	Ser	Gly	Gly	Cys	Pro	Trp	Ser	Leu	Pro	
			165					170						175		
Val	Gly	His	Thr	Leu	Ala	Ser	Val	Ala	Leu							
			180					185								

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